SEQUENCE LISTING

```
<110> Yu, Xuanchuan
      Turner, C. Alexander Jr.
<120> Novel Human Protease and Polynucleotides Encoding the Same
<130> LEX-0298-USA
<150> US 60/261,684
<151> 2001-01-12
<160> 2
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 5289
<212> DNA
<213> homo sapiens
<400> 1
atggaatgct gccgtcgggc aactcctggc acactgctcc tctttctggc tttcctgctc
                                                                        60
                                                                       120
ctgagttcca ggaccgcacg ctccgaggag gaccgggacg gcctatggga tgcctggggc
                                                                       180
ccatggagtg aatgctcacg cacctgcggg ggtggggcct cctactctct gaggcgctgc
ctgagcagca agagctgtga aggaagaaat atccgataca gaacatgcag taatgtggac
                                                                       240
tgcccaccag aagcaggtga tttccgagct cagcaatgct cagctcataa tgatgtcaag
                                                                       300
caccatggcc agttttatga atggcttcct gtgtctaatg accctgacaa cccatgttca
                                                                       360
ctcaagtgcc aagccaaagg aacaaccctg gttgttgaac tagcacctaa ggtcttagat
                                                                       420
ggtacgcgtt gctatacaga atctttggat atgtgcatca gtggtttatg ccaaattgtt
                                                                       480
                                                                       540
ggctgcgatc accagctggg aagcaccgtc aaggaagata actgtggggt ctgcaacgga
                                                                       600
gatgggtcca cctgccggct ggtccgaggg cagtataaat cccagctctc cgcaaccaaa
tcggatgata ctgtggttgc aattccctat ggaagtagac atattcgcct tgtcttaaaa
                                                                       660
ggtcctgatc acttatatct ggaaaccaaa accctccagg ggactaaagg tgaaaacagt
                                                                       720
ctcagctcca caggaacttt ccttgtggac aattctagtg tggacttcca gaaatttcca
                                                                       780
                                                                       840
gacaaagaga tactgagaat ggctggacca ctcacagcag atttcattgt caagattcgt
aactcgggct ccgctgacag tacagtccag ttcatcttct atcaacccat catccaccga
                                                                       900
tggagggaga cggatttctt tccttgctca gcaacctgtg gaggaggtta tcagctgaca
                                                                       960
tcggctgagt gctacgatct gaggagcaac cgtgtggttg ctgaccaata ctgtcactat
                                                                      1020
                                                                      1080
tacccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca
gccagtgacg gatacaagca gatcatgcct tatgacctct accatcccct tcctcggtgg
                                                                      1140
                                                                      1200
gaggccaccc catggaccgc gtgctcctcc tcgtgtgggg ggggcatcca gagccgggca
                                                                      1260
gtttcctgtg tggaggagga catccagggg catgtcactt cagtggaaga gtggaaatgc
atgtacaccc ctaagatgcc catcgcgcag ccctgcaaca tttttgactg ccctaaatgg
                                                                      1320
ctggcacagg agtggtctcc gtgcacagtg acatgtggcc agggcctcag ataccgtgtg
                                                                      1380
                                                                      1440
gtcctctgca tcgaccatcg aggaatgcac acaggaggct gtagcccaaa aacaaagccc
                                                                      1500
cacataaaag aggaatgcat cgtacccact ccctgctata aacccaaaga gaaacttcca
                                                                      1560
gtcgaggcca agttgccatg gttcaaacaa gctcaagagc tagaagaagg agctgctgtg
tcagaggagc cctcgttcat cccagaggcc tggtcggcct gcacagtcac ctgtggtgtg
                                                                      1620
gggacccagg tgcgaatagt caggtgccag gtgctcctgt ctttctctca gtccgtggct
                                                                      1680
                                                                      1740
gacctgccta ttgacgagtg tgaagggccc aagccagcat cccagcgtgc ctgttatgca
ggcccatgca gcggggaaat tcctgagttc aacccagacg agacagatgg gctctttggt
                                                                      1800
ggcctgcagg atttcgacga gctgtatgac tgggagtatg aggggttcac caagtgctcc
                                                                      1860
                                                                      1920
gagtcctgtg gaggaggtgt ccaggaggct gtggtgagct gcttgaacaa acagactcgg
                                                                      1980
gagectgetg aggagaacet gtgegtgaee ageegeegge ceceacaget eetgaagtee
```

2040 tgcaatttgg atccctgccc agcaaggtgg gaaattggca agtggagtcc atgtagtctc 2100 acatgtgggg tcggcctaca gaccagagac gtcttctgca gccacctgct ttccagagag atgaatgaaa cagtcatcct ggctgatgag ctgtgtcgcc agcccaagcc cagcacggtg 2160 caagettgta accgetttaa ttgeeceeca geetggtaee etgeacagtg geageegtgt 2220 tccagaacgt gtggcggggg tgttcagaaa cgtgaggttc tttgcaagca gcgcatggct 2280 gatggcaget teetggaget teetgagace ttetgtteag etteaaaace tgeetgeeag 2340 2400 caagcatgca agaaagatga ctgtcccagc gagtggcttc tctcagactg gacagagtgt tccacaagct gcggggaagg cacccagact cgaagcgcca tttgccgaaa gatgctgaaa 2460 2520 accggectet caacggttgt caattecace etgtgeeege ecetgeettt etetteetee atcaggccct gtatgctggc aacctgtgca aggcccgggc ggccatccac gaagcacagc 2580 2640 ccgcacatcg cggccgccag gaaggtctac atccagactc gcaggcagag gaagctgcac 2700 ttcgtggtgg ggggcttcgc ctacctgctc cccaagacgg cggtggtgct gcgctgcccg 2760 gcgcgcaggg tccgcaagcc cctcatcacc tgggagaagg acggccagca cctcatcagc 2820 tcgacgcacg tcacggtggc ccccttcggc tatctcaaga tccaccgcct caagccctcg 2880 gatgcaggcg tctacacctg ctcagcgggc ccggcccggg agcactttgt gattaagctc 2940 atcggaggca accgcaagct cgtggcccgg cccttgagcc cgagaagtga ggaagaggtg 3000 cttgcgggga ggaagggcgg cccgaaggag gccctgcaga cccacaaaca ccagaacggg 3060 atcttctcca acggcagcaa ggcggagaag cggggcctgg ccgccaaccc ggggagccgc 3120 tacgacgacc tcgtctcccg gctgctggag cagggcggct ggcccggaga gctgctggcc 3180 tcgtgggagg cgcaggactc cgcggaaagg aacacgacct cggaggagga cccgggtgca 3240 gagcaagtgc tcctgcacct gcccttcacc atggtgaccg agcagcggcg cctggacgac atcctgggga acctctccca gcagcccgag gagctgcgcg acctctacag caagcacctg 3300 gtggcccagc tggcccagga gatcttccgc agccacctgg agcaccagga cacgctcctg 3360 3420 aagccctcgg agcgcaggac ttccccagtg actctctcgc ctcataaaca cgtgtctggc ttcagcagct ccctgcggac ctcctccacc ggggacgccg ggggaggctc tcgaaggcca 3480 caccgcaagc ccaccatcct gcgcaagatc tcagcggccc agcagctctc agcctcggag 3540 3600 gtggtcaccc acctggggca gacggtggcc ctggccagcg ggacactgag tgttcttctg 3660 cactgtgagg ccatcggcca cccaaggcct accatcagct gggccaggaa tggagaagaa 3720 gttcagttca gtgacaggat tcttctacag ccagatgatt ccttacagat cttggcacca 3780 gtggaagcag atgtgggttt ctacacttgc aatgccacca atgccttggg atacgactct 3840 gtctccattg ccgtcacatt agcaggaaag ccactagtga aaacgtcacg aatgacagtg atcaacacgg agaagcctgc agtcacagtc gatataggaa gcaccatcaa aacagtgcag 3900 ggagtgaatg tgacaatcaa ctgccaggtt gcaggagtgc ctgaagctga agtcacttgg 3960 4020 ttcaggaata aaagcaaact gggctccccg caccatctgc acgaaggctc cttgctgctc 4080 acaaacgtgt cctcctcgga tcagggcctg tactcctgca gggcggccaa tcttcatgga 4140 gagetgactg agageaceea getgetgate etagateeee eecaagteee cacacagttg gaagacatca gggccttgct cgctgccact ggaccgaacc ttccttcagt gctgacgtct 4200 4260 cctctgggaa cacagctggt cctggatcct gggaattctg ctctccttgg ctgccccatc aaaggtcacc ctgtccctaa tatcacctgg tttcatggtg gtcagccaat tgtcactgcc 4320 4380 acaggactga cgcatcacat cttggcagct ggacagatcc ttcaagttgc aaaccttagc ggtgggtctc aaggggaatt cagctgcctt gctcagaatg aggcaggggt gctcatgcag 4440 4500 aaggcatctt tagtgatcca agattactgg tggtctgtgg acagactggc aacctgctca gcctcctgtg gtaaccgggg ggttcagcag ccccgcttga ggtgcctgct gaacagcacg 4560 gaggtcaacc ctgcccactg cgcagggaag gttcgccctg cggtgcagcc catcgcgtgc 4620 aaccggagag actgcccttc tcggtggatg gtgacctcct ggtctgcctg tacccggagc 4680 4740 tgtgggggag gtgtccagac ccgcagggtg acctgtcaaa agctgaaagc ctctgggatc tccaccctg tgtccaatga catgtgcacc caggtcgcca agcggcctgt ggacacccag 4800 4860 gcctgtaacc agcagctgtg tgtggagtgg gccttctcca gctggggcca gtgcaatggg 4920 ccttgcatcg ggcctcacct agctgtgcaa cacagacaag tcttctgcca gacacgggat 4980 ggcatcacct taccatcaga gcagtgcagt gctcttccga ggcctgtgag cacccagaac 5040 tgctggtcag aggcctgcag tgtacactgg agagtcagcc tgtggaccct gtgcacagct 5100 acctgtggca actacggctt ccagtcccgg cgtgtggagt gtgtgcatgc ccgcaccaac 5160 aaggcagtgc ctgagcacct gtgctcctgg gggccccggc ctgccaactg gcagcgctgc 5220 aacatcaccc catgtgaaaa catggagtgc agagacacca ccaggtactg cgagaaggtg 5280 aaacagctga aactctgcca actcagccag tttaaatctc gctgctgtgg aacttgtggc 5289 aaagcgtga

<210> 2 <211> 1762 <212> PRT <213> homo sapiens <400> 2 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu Ala Phe Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg 25 Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr 40 Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys 55 Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp 70 75 Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln Cys Ser Ala His 90 Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp Leu Pro Val Ser 105 Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr 115 120 125 Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys 135 140 Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Gln Ile Val 150 155 Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly 165 170 Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr 180 185 Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile 200 Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His 215 220 Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser 230 235 Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe 245 250 Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr 265 Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr 280 Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu Thr 295 300 Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Tyr Gln Leu Thr 310 315 Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln 325 330 Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln 345 Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile 360 365 Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro 375 380

Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala 395 390 Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu 410 405 Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys 425 Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys 445 440 Thr Val Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile 460 455 Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro 475 470 His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys 490 485 Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln Ala Gln 505 Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser Phe Ile Pro 525 520 Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val Gly Thr Gln Val 535 540 Arg Ile Val Arg Cys Gln Val Leu Leu Ser Phe Ser Gln Ser Val Ala 555 550 Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro Lys Pro Ala Ser Gln Arg 570 565 Ala Cys Tyr Ala Gly Pro Cys Ser Gly Glu Ile Pro Glu Phe Asn Pro 585 Asp Glu Thr Asp Gly Leu Phe Gly Gly Leu Gln Asp Phe Asp Glu Leu 605 600 Tyr Asp Trp Glu Tyr Glu Gly Phe Thr Lys Cys Ser Glu Ser Cys Gly 620 615 Gly Gly Val Gln Glu Ala Val Val Ser Cys Leu Asn Lys Gln Thr Arg 635 630 Glu Pro Ala Glu Glu Asn Leu Cys Val Thr Ser Arg Arg Pro Pro Gln 645 650 Leu Leu Lys Ser Cys Asn Leu Asp Pro Cys Pro Ala Arg Trp Glu Ile 660 665 Gly Lys Trp Ser Pro Cys Ser Leu Thr Cys Gly Val Gly Leu Gln Thr 685 680 Arg Asp Val Phe Cys Ser His Leu Leu Ser Arg Glu Met Asn Glu Thr 700 695 Val Ile Leu Ala Asp Glu Leu Cys Arg Gln Pro Lys Pro Ser Thr Val 715 710 Gln Ala Cys Asn Arg Phe Asn Cys Pro Pro Ala Trp Tyr Pro Ala Gln 730 725 Trp Gln Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Lys Arg Glu 745 Val Leu Cys Lys Gln Arg Met Ala Asp Gly Ser Phe Leu Glu Leu Pro 760 Glu Thr Phe Cys Ser Ala Ser Lys Pro Ala Cys Gln Gln Ala Cys Lys 780 775 Lys Asp Asp Cys Pro Ser Glu Trp Leu Leu Ser Asp Trp Thr Glu Cys 790 795 Ser Thr Ser Cys Gly Glu Gly Thr Gln Thr Arg Ser Ala Ile Cys Arg 810 805 Lys Met Leu Lys Thr Gly Leu Ser Thr Val Val Asn Ser Thr Leu Cys 825 820

Pro Pro Leu Pro Phe Ser Ser Ser Ile Arg Pro Cys Met Leu Ala Thr 840 Cys Ala Arg Pro Gly Arg Pro Ser Thr Lys His Ser Pro His Ile Ala 855 860 Ala Ala Arg Lys Val Tyr Ile Gln Thr Arg Arg Gln Arg Lys Leu His 870 875 Phe Val Val Gly Gly Phe Ala Tyr Leu Leu Pro Lys Thr Ala Val Val 885 890 895 Leu Arg Cys Pro Ala Arg Arg Val Arg Lys Pro Leu Ile Thr Trp Glu 905 Lys Asp Gly Gln His Leu Ile Ser Ser Thr His Val Thr Val Ala Pro 920 915 Phe Gly Tyr Leu Lys Ile His Arg Leu Lys Pro Ser Asp Ala Gly Val 935 Tyr Thr Cys Ser Ala Gly Pro Ala Arg Glu His Phe Val Ile Lys Leu 955 950 Ile Gly Gly Asn Arg Lys Leu Val Ala Arg Pro Leu Ser Pro Arg Ser 970 Glu Glu Val Leu Ala Gly Arg Lys Gly Gly Pro Lys Glu Ala Leu 980 985 Gln Thr His Lys His Gln Asn Gly Ile Phe Ser Asn Gly Ser Lys Ala 1000 Glu Lys Arg Gly Leu Ala Ala Asn Pro Gly Ser Arg Tyr Asp Asp Leu 1010 1015 1020 Val Ser Arg Leu Leu Glu Gln Gly Gly Trp Pro Gly Glu Leu Leu Ala 1030 1035 Ser Trp Glu Ala Gln Asp Ser Ala Glu Arg Asn Thr Thr Ser Glu Glu 1045 1050 Asp Pro Gly Ala Glu Gln Val Leu Leu His Leu Pro Phe Thr Met Val 1070 1060 1065 Thr Glu Gln Arg Arg Leu Asp Asp Ile Leu Gly Asn Leu Ser Gln Gln 1080 Pro Glu Glu Leu Arg Asp Leu Tyr Ser Lys His Leu Val Ala Gln Leu 1095 1100 Ala Gln Glu Ile Phe Arg Ser His Leu Glu His Gln Asp Thr Leu Leu 1110 1115 Lys Pro Ser Glu Arg Arg Thr Ser Pro Val Thr Leu Ser Pro His Lys 1125 1130 1135 His Val Ser Gly Phe Ser Ser Ser Leu Arg Thr Ser Ser Thr Gly Asp 1140 1145 1150 Ala Gly Gly Ser Arg Arg Pro His Arg Lys Pro Thr Ile Leu Arg 1155 1160 1165 Lys Ile Ser Ala Ala Gln Gln Leu Ser Ala Ser Glu Val Val Thr His 1170 1175 1180 Leu Gly Gln Thr Val Ala Leu Ala Ser Gly Thr Leu Ser Val Leu Leu 1190 1195 His Cys Glu Ala Ile Gly His Pro Arg Pro Thr Ile Ser Trp Ala Arg 1205 1210 Asn Gly Glu Glu Val Gln Phe Ser Asp Arg Ile Leu Leu Gln Pro Asp 1220 1225 Asp Ser Leu Gln Ile Leu Ala Pro Val Glu Ala Asp Val Gly Phe Tyr 1240 1245 Thr Cys Asn Ala Thr Asn Ala Leu Gly Tyr Asp Ser Val Ser Ile Ala 1255 1260 Val Thr Leu Ala Gly Lys Pro Leu Val Lys Thr Ser Arg Met Thr Val 1275 1270

Ile Asn Thr Glu Lys Pro Ala Val Thr Val Asp Ile Gly Ser Thr Ile 1290 1285 Lys Thr Val Gln Gly Val Asn Val Thr Ile Asn Cys Gln Val Ala Gly 1300 1305 1310 Val Pro Glu Ala Glu Val Thr Trp Phe Arg Asn Lys Ser Lys Leu Gly 1315 1320 1325 Ser Pro His His Leu His Glu Gly Ser Leu Leu Thr Asn Val Ser 1335 1340 Ser Ser Asp Gln Gly Leu Tyr Ser Cys Arg Ala Ala Asn Leu His Gly 1350 1355 1360 Glu Leu Thr Glu Ser Thr Gln Leu Leu Ile Leu Asp Pro Pro Gln Val 1370 1365 Pro Thr Gln Leu Glu Asp Ile Arg Ala Leu Leu Ala Ala Thr Gly Pro 1380 1385 1390 Asn Leu Pro Ser Val Leu Thr Ser Pro Leu Gly Thr Gln Leu Val Leu 1395 1400 1405 Asp Pro Gly Asn Ser Ala Leu Leu Gly Cys Pro Ile Lys Gly His Pro 1410 1415 1420 Val Pro Asn Ile Thr Trp Phe His Gly Gly Gln Pro Ile Val Thr Ala 1425 1430 1435 1440 Thr Gly Leu Thr His His Ile Leu Ala Ala Gly Gln Ile Leu Gln Val 1445 1450 1455 Ala Asn Leu Ser Gly Gly Ser Gln Gly Glu Phe Ser Cys Leu Ala Gln 1465 1470 1460 Asn Glu Ala Gly Val Leu Met Gln Lys Ala Ser Leu Val Ile Gln Asp 1480 Tyr Trp Trp Ser Val Asp Arg Leu Ala Thr Cys Ser Ala Ser Cys Gly 1495 1490 1500 Asn Arg Gly Val Gln Gln Pro Arg Leu Arg Cys Leu Leu Asn Ser Thr 1510 1515 Glu Val Asn Pro Ala His Cys Ala Gly Lys Val Arg Pro Ala Val Gln 1525 1530 Pro Ile Ala Cys Asn Arg Arg Asp Cys Pro Ser Arg Trp Met Val Thr 1540 1545 1550 Ser Trp Ser Ala Cys Thr Arg Ser Cys Gly Gly Val Gln Thr Arg 1555 1560 Arg Val Thr Cys Gln Lys Leu Lys Ala Ser Gly Ile Ser Thr Pro Val 1570 1575 1580 Ser Asn Asp Met Cys Thr Gln Val Ala Lys Arg Pro Val Asp Thr Gln 1585 1590 1595 1600 Ala Cys Asn Gln Gln Leu Cys Val Glu Trp Ala Phe Ser Ser Trp Gly 1605 1610 1615 Gln Cys Asn Gly Pro Cys Ile Gly Pro His Leu Ala Val Gln His Arg 1620 1625 1630 Gln Val Phe Cys Gln Thr Arg Asp Gly Ile Thr Leu Pro Ser Glu Gln 1640 Cys Ser Ala Leu Pro Arg Pro Val Ser Thr Gln Asn Cys Trp Ser Glu 1650 1655 1660 Ala Cys Ser Val His Trp Arg Val Ser Leu Trp Thr Leu Cys Thr Ala 1670 1675 Thr Cys Gly Asn Tyr Gly Phe Gln Ser Arg Arg Val Glu Cys Val His 1685 1690 1695 Ala Arg Thr Asn Lys Ala Val Pro Glu His Leu Cys Ser Trp Gly Pro 1700 1705 1710 Arg Pro Ala Asn Trp Gln Arg Cys Asn Ile Thr Pro Cys Glu Asn Met 1720 1725

Glu Cys Arg Asp Thr Thr Arg Tyr Cys Glu Lys Val Lys Gln Leu Lys 1730 Leu Cys Gln Leu Ser Gln Phe Lys Ser Arg Cys Cys Gly Thr Cys Gly 1745 Lys Ala

7 KA 3